

0590  
 06/25 OIPE  
 #3

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/767,215

DATE: 07/02/2001  
 TIME: 16:52:23

Input Set : A:\07334-142001.txt  
 Output Set: N:\CRF3\07022001\I767215.raw

ENTERED

4 <110> APPLICANT: Bertin, John  
 6 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 7 PROTEIN FAMILY AND USES THEREOF  
 9 <130> FILE REFERENCE: 07334-142001  
 11 <140> CURRENT APPLICATION NUMBER: 09/767,215  
 12 <141> CURRENT FILING DATE: 2001-01-22  
 14 <150> PRIOR APPLICATION NUMBER: 60/181,159  
 15 <151> PRIOR FILING DATE: 2000-02-09  
 17 <160> NUMBER OF SEQ ID NOS: 10  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 3931  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (207)...(3218)  
 30 <400> SEQUENCE: 1  
 31 attcggtctcg agttcacctg gtgctgcttt gacttcaggc tcttccttct gcccagctcc 60  
 32 gtccccaccca gcagcccgca gagaaaaggag gcagctggca ccacactggg ctttggagac 120  
 33 actgcgggga ctgtggaccc caccctgctg cacggagctc ctgcaaaagc aaacctgaga 180  
 34 accttgggtc ctcccaagcgc ccagcc atg ggg gaa ctg tgc cgc agg gac tcc 233  
 35 Met Gly Glu Leu Cys Arg Arg Asp Ser  
 36 1 5  
 38 gca ctc acg gca ctg gac gag aca ctg tgg gag atg atg gag agc 281  
 39 Ala Leu Thr Ala Leu Asp Glu Glu Thr Leu Trp Glu Met Met Glu Ser  
 40 10 15 20 25  
 42 cac cgc cac agg atc gta cgc tgc atc tgc ccc agc cgc ctc acc ccc 329  
 43 His Arg His Arg Ile Val Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro  
 44 30 35 40  
 46 tac ctg cgc cag gcc aag gtg ctg tgc cag ctg gac gag gag gag gtg 377  
 47 Tyr Leu Arg Gln Ala Lys Val Leu Cys Gln Leu Asp Glu Glu Val  
 48 45 50 55  
 50 ctg cac agc ccc cgg ctc acc aac agc gcc atg cgg gcc ggg cac ttg 425  
 51 Leu His Ser Pro Arg Leu Thr Asn Ser Ala Met Arg Ala Gly His Leu  
 52 60 65 70  
 54 ctg gat ttg ctg aag act cga ggg aag aac ggg gcc atc gcc ttc ctg 473  
 55 Leu Asp Leu Leu Lys Thr Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu  
 56 75 80 85  
 58 gag agc ctg aag ttc cac aac cct gac gtc tac acc ctg gtc acc ggg 521  
 59 Glu Ser Leu Lys Phe His Asn Pro Asp Val Tyr Thr Leu Val Thr Gly  
 60 90 95 100 105  
 62 ctg cag cct gat gtt gac ttc agt aac ttt agc ggt ctc atg gag aca 569  
 63 Leu Gln Pro Asp Val Asp Phe Ser Asn Phe Ser Gly Leu Met Glu Thr  
 64 110 115 120  
 66 tcc aag ctg acc gag tgc ctg gct ggg gcc atc ggc agc ctg cag gag 617  
 67 Ser Lys Leu Thr Glu Cys Leu Ala Gly Ala Ile Gly Ser Leu Gln Glu

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68	125	130	135	
70	gag ctg aac cag gaa aag ggg cag aag gag gtg ctg ctg cgg cgg tgc			665
71	Glu Leu Asn Gln Glu Lys Gly Gln Lys Glu Val Leu Leu Arg Arg Cys			
72	140	145	150	
74	cag cag ctg cag gag cac ctg ggc ctg gcc gag acc cgt gcc gag ggc			713
75	Gln Gln Leu Gln Glu His Leu Gly Leu Ala Glu Thr Arg Ala Glu Gly			
76	155	160	165	
78	ctg cac cag ctg gag gct gac cac agc cgc atg aag cgt gag gtt agc			761
79	Leu His Gln Leu Glu Ala Asp His Ser Arg Met Lys Arg Glu Val Ser			
80	170	175	180	185
82	gca cac ttc cat gag gtg ctg agg ctg aag gac gag atg ctc agc ctc			809
83	Ala His Phe His Glu Val Leu Arg Leu Lys Asp Glu Met Leu Ser Leu			
84	190	195	200	
86	tcg ctg cac tat agc aat gcg ctg cag gag aag gag ctg gcc gcc tca			857
87	Ser Leu His Tyr Ser Asn Ala Leu Gln Glu Lys Glu Leu Ala Ala Ser			
88	205	210	215	
90	cgc tgc cgc agc ctg cag gag ctg tat cta ctg aag cag gag ctg			905
91	Arg Cys Arg Ser Leu Gln Glu Leu Tyr Leu Leu Lys Gln Glu Leu			
92	220	225	230	
94	cag cga gcc aac atg gtt tcc tcc tgt gag ctg gaa ttg caa gag cag			953
95	Gln Arg Ala Asn Met Val Ser Ser Cys Glu Leu Glu Leu Gln Glu Gln			
96	235	240	245	
98	tcc ctg agg aca gcc agc gac cag gag tcc ggg gat gag gag ctg aac			1001
99	Ser Leu Arg Thr Ala Ser Asp Gln Glu Ser Gly Asp Glu Glu Leu Asn			
100	250	255	260	265
102	cgc ctg aag gag aat gag aaa ctg cgc tgc ctg act ttc agc ctg			1049
103	Arg Leu Lys Glu Glu Asn Glu Lys Leu Arg Ser Leu Thr Phe Ser Leu			
104	270	275	280	
106	gcg gag aag gac att ctg gag cag agc ctg gac gag gcg cgg ggg agc			1097
107	Ala Glu Lys Asp Ile Leu Glu Gln Ser Leu Asp Glu Ala Arg Gly Ser			
108	285	290	295	
110	cga cag gag ctg gtg gag cgc atc cac tgc ctg cgg gag cgg gcc gtg			1145
111	Arg Gln Glu Leu Val Glu Arg Ile His Ser Leu Arg Glu Arg Ala Val			
112	300	305	310	
114	gct gcc gag agg cag cga gag cag tac tgg gaa gag aag gaa cag acc			1193
115	Ala Ala Glu Arg Gln Arg Glu Gln Tyr Trp Glu Glu Lys Glu Gln Thr			
116	315	320	325	
118	ctg ctg cag ttc cag aag agt aag atg gcc tgc caa ctc tac agg gag			1241
119	Leu Leu Gln Phe Gln Lys Ser Lys Met Ala Cys Gln Leu Tyr Arg Glu			
120	330	335	340	345
122	aag gtg aat gcg ctg cag gcc cag gtg tgc gag ctg cag aag gag cga			1289
123	Lys Val Asn Ala Leu Gln Ala Gln Val Cys Glu Leu Gln Lys Glu Arg			
124	350	355	360	
126	gac cag gcg tac tcc gcg agg gac agt gct cag agg gag att tcc cag			1337
127	Asp Gln Ala Tyr Ser Ala Arg Asp Ser Ala Gln Arg Glu Ile Ser Gln			
128	365	370	375	
130	agc ctg gtg gag aag gac tcc ctc cgc agg cag gtg ttc gag ctg acg			1385
131	Ser Leu Val Glu Lys Asp Ser Leu Arg Arg Gln Val Phe Glu Leu Thr			
132	380	385	390	

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134 gac cag gtc tgc gag ctg cgc aca cag ctt cgc cag ctg cag gca gag	1433
135 Asp Gln Val Cys Glu Leu Arg Thr Gln Leu Arg Gln Leu Gln Ala Glu	
136 395 400 405	
138 cct ccg ggt gtg ctc aag cag gaa gcc agg acc agg gag ccc tgt cca	1481
139 Pro Pro Gly Val Leu Lys Gln Glu Ala Arg Thr Arg Glu Pro Cys Pro	
140 410 415 420 425	
142 cgg gag aag cag cgg ctg gtg cgg atg cat gcc atc tgc ccc aga gac	1529
143 Arg Glu Lys Gln Arg Leu Val Arg Met His Ala Ile Cys Pro Arg Asp	
144 430 435 440	
146 gac agc gac tgc agc ctc gtc agc tcc aca gag tct cag ctc ttg tcg	1577
147 Asp Ser Asp Cys Ser Leu Val Ser Ser Thr Glu Ser Gln Leu Leu Ser	
148 445 450 455	
150 gac ctg agt gcc acg tcc agc cgc gag ctg gtg gac agc ttc cgc tcc	1625
151 Asp Leu Ser Ala Thr Ser Ser Arg Glu Leu Val Asp Ser Phe Arg Ser	
152 460 465 470	
154 agc agc ccc gcg ccc ccc agc cag cag tcc ctg tac aag cgg gtg gcc	1673
155 Ser Ser Pro Ala Pro Pro Ser Gln Gln Ser Leu Tyr Lys Arg Val Ala	
156 475 480 485	
158 gag gac ttc ggg gaa gaa ccc tgg tct ttc agc agc tgc ctg gag atc	1721
159 Glu Asp Phe Gly Glu Glu Pro Trp Ser Phe Ser Ser Cys Leu Glu Ile	
160 490 495 500 505	
162 ccc gag gga gac ccc gga gcc ctg ccc gga gct aag gca ggc gac cca	1769
163 Pro Glu Gly Asp Pro Gly Ala Leu Pro Gly Ala Lys Ala Gly Asp Pro	
164 510 515 520	
166 cac ctg gat tat gag ctc cta gac acg gca gac ctt ccg cag ctg gaa	1817
167 His Leu Asp Tyr Glu Leu Leu Asp Thr Ala Asp Leu Pro Gln Leu Glu	
168 525 530 535	
170 agc agc ctg cag cca gtc tcc cct gga agg ctt gat gtc tcg gag agc	1865
171 Ser Ser Leu Gln Pro Val Ser Pro Gly Arg Leu Asp Val Ser Glu Ser	
172 540 545 550	
174 ggc gtc ctc atg cgg cgg agg cca gcc cgc agg atc ctg agc cag gtc	1913
175 Gly Val Leu Met Arg Arg Arg Pro Ala Arg Arg Ile Leu Ser Gln Val	
176 555 560 565	
178 acc atg ctg gcg ttc cag ggg gat gca ttg ctg gag cag atc agc gtc	1961
179 Thr Met Leu Ala Phe Gln Gly Asp Ala Leu Leu Glu Gln Ile Ser Val	
180 570 575 580 585	
182 atc ggc ggg aac ctc acg ggc atc ttc atc cac cgg gtc acc ccc ggc	2009
183 Ile Gly Gly Asn Leu Thr Gly Ile Phe Ile His Arg Val Thr Pro Gly	
184 590 595 600	
186 tcg gcg gcg gac cag atg gcc ttg cgc ccc ggc acc cag att gtg atg	2057
187 Ser Ala Ala Asp Gln Met Ala Leu Arg Pro Gly Thr Gln Ile Val Met	
188 605 610 615	
190 gtt gat tac gaa gcc tca gag ccc ttg ttc aag gca gtc ctg gag gac	2105
191 Val Asp Tyr Glu Ala Ser Glu Pro Leu Phe Lys Ala Val Leu Glu Asp	
192 620 625 630	
194 acg acc ctg gag gag gcc gtg ggg ctt ctc agg agg gtg gac ggc ttc	2153
195 Thr Thr Leu Glu Ala Val Gly Leu Leu Arg Arg Val Asp Gly Phe	
196 635 640 645	
198 tgc tgc ctg tct gtg aag gtc aac acg gac ggt tat aag agg cta ctc	2201

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199	Cys	Cys	Leu	Ser	Val	Lys	Val	Asn	Thr	Asp	Gly	Tyr	Lys	Arg	Leu	Leu	
200	650				655					660					665		
202	cag	gac	ctg	gag	gcc	aaa	gtg	gcg	acc	tcg	ggg	gac	tca	ttc	tac	atc	2249
203	Gln	Asp	Leu	Glu	Ala	Lys	Val	Ala	Thr	Ser	Gly	Asp	Ser	Phe	Tyr	Ile	
204					670					675					680		
206	cgg	gtc	aac	ctg	gcc	atg	gag	ggc	agg	gcc	aaa	ggg	gag	ctg	cag	gtg	2297
207	Arg	Val	Asn	Leu	Ala	Met	Glu	Gly	Arg	Ala	Lys	Gly	Glu	Leu	Gln	Val	
208					685					690					695		
210	cat	tgc	aac	gag	gtc	ctg	cac	gtc	acc	gac	acc	atg	ttc	cag	ggc	tgc	2345
211	His	Cys	Asn	Glu	Val	Leu	His	Val	Thr	Asp	Thr	Met	Phe	Gln	Gly	Cys	
212					700					705					710		
214	ggc	tgc	tgg	cat	gcc	cac	cgc	gtg	aac	tct	tac	acc	atg	aag	gat	act	2393
215	Gly	Cys	Trp	His	Ala	His	Arg	Val	Asn	Ser	Tyr	Thr	Met	Lys	Asp	Thr	
216					715					720					725		
218	gcc	gcf	cac	ggc	acc	atc	ccc	aac	tac	tcc	agg	gct	cag	cag	cag	ctc	2441
219	Ala	Ala	His	Gly	Thr	Ile	Pro	Asn	Tyr	Ser	Arg	Ala	Gln	Gln	Gln	Leu	
220					730					735					740		745
222	ata	gcc	ctc	atc	cag	gac	atg	act	cag	cag	tgc	acc	gtg	acc	cgc	aag	2489
223	Ile	Ala	Leu	Ile	Gln	Asp	Met	Thr	Gln	Gln	Cys	Thr	Val	Thr	Arg	Lys	
224					750					755					760		
226	cca	tct	tct	ggg	gga	cca	cag	aag	ctg	gtc	cgc	atc	gtc	agt	atg	gac	2537
227	Pro	Ser	Ser	Gly	Gly	Pro	Gln	Lys	Leu	Val	Arg	Ile	Val	Ser	Met	Asp	
228					765					770					775		
230	aaa	gcc	aag	gcc	agc	cct	ctg	cgt	ttg	tcc	ttt	gac	agg	ggc	cag	ttg	2585
231	Lys	Ala	Lys	Ala	Ser	Pro	Leu	Arg	Leu	Ser	Phe	Asp	Arg	Gly	Gln	Leu	
232					780					785					790		
234	gac	ccc	agc	agg	atg	gag	ggc	tcc	agc	acg	tgc	ttc	tgg	gcc	gag	agc	2633
235	Asp	Pro	Ser	Arg	Met	Glu	Gly	Ser	Ser	Thr	Cys	Phe	Trp	Ala	Glu	Ser	
236					795					800					805		
238	tgc	ctc	acc	ctg	gtg	ccc	tat	acc	ctg	gtg	tgg	ccc	cat	cga	ccc	gcc	2681
239	Cys	Leu	Thr	Leu	Val	Pro	Tyr	Thr	Leu	Val	Trp	Pro	His	Arg	Pro	Ala	
240					810					815					820		825
242	cgg	ccc	cgg	cct	gtg	ctc	ctc	gtg	ccc	agg	gcf	gtt	ggg	aag	atc	ctg	2729
243	Arg	Pro	Arg	Pro	Val	Leu	Leu	Val	Pro	Arg	Ala	Val	Gly	Lys	Ile	Leu	
244					830					835					840		
246	agc	gag	aaa	ctg	tgc	ctc	ctc	caa	ggg	ttt	aag	aag	tgc	ctg	gca	gag	2777
247	Ser	Glu	Lys	Leu	Cys	Leu	Leu	Gln	Gly	Phe	Lys	Lys	Cys	Leu	Ala	Glu	
248					845					850					855		
250	tac	ttg	agc	cag	gag	gag	tat	gag	gcc	tgg	agc	cag	aga	ggg	gac	atc	2825
251	Tyr	Leu	Ser	Gln	Glu	Glu	Tyr	Glu	Ala	Trp	Ser	Gln	Arg	Gly	Asp	Ile	
252					860					865					870		
254	atc	cag	gag	gga	gag	gtg	tcc	ggg	ggc	cgc	tgc	tgg	gtg	acc	cgc	cat	2873
255	Ile	Gln	Glu	Gly	Glu	Val	Ser	Gly	Gly	Arg	Cys	Trp	Val	Thr	Arg	His	
256					875					880					885		
258	gct	gtg	gag	tcc	ctc	atg	gaa	aag	aac	acc	cat	gcc	ctc	ctg	gac	gtc	2921
259	Ala	Val	Glu	Ser	Leu	Met	Glu	Lys	Asn	Thr	His	Ala	Leu	Leu	Asp	Val	
260					890					895					900		905
262	cag	ctg	gac	agt	gtc	tgc	acc	ctg	cac	agg	atg	gac	atc	ttc	ccc	atc	2969
263	Gln	Leu	Asp	Ser	Val	Cys	Thr	Leu	His	Arg	Met	Asp	Ile	Phe	Pro	Ile	

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264	910	915	920	
266	gtc atc cac gtc tct gtc aac gag aag atg gca aag aag ctc aag aag			3017
267	Val Ile His Val Ser Val Asn Glu Lys Met Ala Lys Lys Leu Lys Lys			
268	925	930	935	
270	ggc cta cag cgg ttg ggc acc tca gag gag cag ctc ctg gag gct gcg			3065
271	Gly Leu Gln Arg Leu Gly Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala			
272	940	945	950	
274	agg cag gag gag gga gac ctg gac cgg gcg ccc tgt cta tac agc agc			3113
275	Arg Gln Glu Glu Gly Asp Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser			
276	955	960	965	
278	ctg gct cct gac ggc tgg agc gac ctg gac ggc ctg ctc agc tgt gtc			3161
279	Leu Ala Pro Asp Gly Trp Ser Asp Leu Asp Gly Leu Leu Ser Cys Val			
280	970	975	980	985
282	cgc cag gcc atc gcc gac gag cag aag aag gtg gtg tgg acg gag cag			3209
283	Arg Gln Ala Ile Ala Asp Glu Gln Lys Lys Val Val Trp Thr Glu Gln			
284	990	995	1000	
286	agc ccc cga tgatgcaccc tgcccttcc cggactgtg gggcttctg			3258
287	Ser Pro Arg			
290	tgtgcctgtt aatgcagtcc tggcctcag cccaggccct cttggcacag ctgtgggctc			3318
291	cttggcacat gaggccggct ctcccccactg gctgggtct aaccttgaac cctcaccacg			3378
292	tgcaggtcac acacagtcaa gccacttcta actgcacact tttctgttga aacatcttca			3438
293	cccttacca ggcttggcat ggtctgaact ggaaaccctg agaatgttc tgca tagga			3498
294	caggagggac atcttccat gccttcccta gaaccggagg cccggactt ctctggaaaa			3558
295	ccgcctgtct gcaggcccga ttcaaatcta tggggctgc acttccctt tacatggaa			3618
296	tgtgtcaaag gctttggag tgacaaaaag cacagaggca gcgggtggg cgcctgggtg			3678
297	gtccccaagg tcgctgccac ctttgcctt ggcagaggca taagccaca tatgtgtga			3738
298	cgctggccac ctttctcag cttctgaggc tgcgtatgcct caggaactcc agtttacaga			3798
299	gaccagtgtg tttacttcta aataaagctt ctgggtggtg gagacggtaa tttcagttggg			3858
300	tctgtcccc gtggcccttg tgcctgttgc gtgggggtgt cccagagaag cctggcacca			3918
301	gtaccccccgt caa			3931
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304	<211> LENGTH: 1004			
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306	<213> ORGANISM: Homo sapiens			
308	<400> SEQUENCE: 2			
309	Met Gly Glu Leu Cys Arg Arg Asp Ser Ala Leu Thr Ala Leu Asp Glu			
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311	Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val Arg			
312	20 25 30			
313	Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys Val			
314	35 40 45			
315	Leu Cys Gln Leu Asp Glu Glu Val Leu His Ser Pro Arg Leu Thr			
316	50 55 60			
317	Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr Arg			
318	65 70 75 80			
319	Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His Asn			
320	85 90 95			
321	Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln Pro Asp Val Asp Phe			
322	100 105 110			

**VERIFICATION SUMMARY**

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